



9207..4.ST25.txt
SEQUENCE LISTING

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Miller, Edward S.
Kelly, Robert M.

<120> METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-CONTAINING
OLIGOSACCHARIDES IN COMPLEX MIXTURES

<130> 9207.4

<150> US 60/220,211

<151> 2000-07-22

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1659

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1659)

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1 5 10 15

48

gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc
Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly
20 25 30

96

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tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt	144
Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val	
35 40 45	
ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc	192
Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser	
50 55 60	
tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa	240
Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu	
65 70 75 80	
ata gat ccg aac tgg aga tac acc gct tgc gtg gtg ccc gat gta ctt	288
Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu	
85 90 95	
gaa agg aac ctc cag agc gac tat ttc gtg gct gaa gaa gga aaa gtg	336
Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val	
100 105 110	
tac ggt ttt ctg agt tgc aaa atc gca cat cct ttc ttc gct gtg gaa	384
Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu	
115 120 125	
gat ggg gaa ctt gtg gca tac ctc gaa tat ttc gat gtc gag ttc gac	432
Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp	
130 135 140	
gac ttt gtt cct ctt gaa cct ctc gtt gta ctc gag gat ccc aac aca	480
Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr	
145 150 155 160	
ccc ctt ctt ctg gag aaa tac gcg gaa ctc gtc gga atg gaa aac aac	528
Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn	
165 170 175	
gcg aga gtt cca aaa cac aca ccc act gga tgg tgc agc tgg tac cat	576
Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His	
180 185 190	
tac ttc ctt gat ctc acc tgg gaa gag acc ctc aag aac ctg aag ctc	624
Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu	
195 200 205	
gcg aag aat ttc ccg ttc gag gtc ttc cag ata gac gac gcc tac gaa	672
Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu	
210 215 220	
aag gac ata ggt gac tgg ctc gtg aca aga gga gac ttt cca tcg gtg	720
Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val	
225 230 235 240	
gaa gag atg gca aaa gtt ata gcg gaa aac ggt ttc atc ccg ggc ata	768
Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile	
245 250 255	
tgg acc gcc ccg ttc agt gtt tct gaa acc tcg gat gta ttc aac gaa	816
Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu	
260 265 270	
cat ccg gac tgg gta gtg aag gaa aac gga gag ccg aag atg gct tac	864
His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr	

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280

aga aac tgg aac aaa aag ata tac gcc ctc gat ctt tcg aaa gat gag Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu 290 295 300	912
gtt ctg aac tgg ctt ttc gat ctc ttc tca tct ctg aga aag atg ggc Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly 305 310 315 320	960
tac agg tac ttc aag atc gac ttt ctc ttc gcg ggt gcc gtt cca gga Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly 325 330 335	1008
gaa aga aaa aag aac ata aca cca att cag gcg ttc aga aaa ggg att Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile 340 345 350	1056
gag acg atc aga aaa gcg gtg gga gaa gat tct ttc atc ctc gga tgc Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys 355 360 365	1104
ggc tct ccc ctt ctt ccc gca gtg gga tgc gtc gac ggg atg agg ata Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile 370 375 380	1152
gga cct gac act gcg ccg ttc tgg gga gaa cat ata gaa gac aac gga Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly 385 390 400	1200
gct ccc gct gca aga tgg gcg ctg aga aac gcc ata acg agg tac ttc Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe 405 410 415	1248
atg cac gac agg ttc tgg ctg aac gac ccc gac tgt ctg ata ctg aga Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg 420 425 430	1296
gag gag aaa acg gat ctc aca cag aag gaa aag gag ctc tac tcg tac Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr 435 440 445	1344
acg tgt gga gtg ctc gac aac atg atc ata gaa agc gat gat ctc tcg Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser 450 455 460	1392
ctc gtc aga gat cat gga aaa aag gtt ctg aaa gaa acg ctc gaa ctc Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu 465 470 475 480	1440
ctc ggt gga aga cca cgg gtt caa aac atc atg tcg gag gat ctg aga Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg 485 490 495	1488
tac gag atc gtc tcg tct ggc act ctc tca gga aac gtc aag atc gtg Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val 500 505 510	1536
gtc gat ctg aac agc aga gag tac cac ctg gaa aaa gaa gga aag tcc Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser 515 520 525	1584
tcc ctg aaa aaa aga gtc gtc aaa aga gaa gac gga aga aac ttc tac	1632

Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
 530 535 540

ttc tac gaa gag ggt gag aga gaa tga
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 545 550

1659

<210> 2

<211> 552

<212> PRT

<213> Thermotoga maritima

<400> 2

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Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly
 20 25 30

Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
 35 40 45

Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
 50 55 60

Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
 65 70 75 80

Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
 85 90 95

Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val
 100 105 110

Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu
 115 120 125

Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp
 130 135 140

Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr
 145 150 155 160

Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn
 165 170 175

Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His
 180 185 190
 Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu
 195 200 205
 Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu
 210 215 220
 Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val
 225 230 235 240
 Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile
 245 250 255
 Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu
 260 265 270
 His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
 275 280 285
 Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
 290 295 300
 Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
 305 310 315 320
 Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
 325 330 335
 Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
 340 345 350
 Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
 355 360 365
 Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
 370 375 380
 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
 385 390 395 400
 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
 405 410 415
 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
 420 425 430

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Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
 435 440 445

Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
 450 455 460

Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
 465 470 475 480

Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
 485 490 495

Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
 500 505 510

Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
 515 520 525

Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
 530 535 540

Phe Tyr Glu Glu Gly Glu Arg Glu
 545 550